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1600

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/606,740A

DATE: 03/22/2002 P6

TIME: 14:08:15

Input Set : F:\seqlistcorrected.txt

Output Set: N:\CRF3\03222002\I606740A.raw

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3 <110> APPLICANT: Pompejus, Markus  
4 Kroger, Burkhard  
5 Schroder, Hartwig  
6 Zelder, Oskar  
7 Haberhauer, Gregor  
9 <120> TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
10 METABOLIC PATHWAY PROTEINS  
12 <130> FILE REFERENCE: BGI-121CP  
14 <140> CURRENT APPLICATION NUMBER: 09/606,740A  
15 <141> CURRENT FILING DATE: 2000-06-23  
17 <150> PRIOR APPLICATION NUMBER: 60/141,031  
18 <151> PRIOR FILING DATE: 1999-06-25  
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## RAW SEQUENCE LISTING

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TIME: 14:08:15

Input Set : F:\seqlistcorrected.txt

Output Set: N:\CRF3\03222002\I606740A.raw

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191 <160> NUMBER OF SEQ ID NOS: 1158
193 <210> SEQ ID NO: 1
194 <211> LENGTH: 948
195 <212> TYPE: DNA
196 <213> ORGANISM: Corynebacterium glutamicum
198 <220> FEATURE:
199 <221> NAME/KEY: CDS
200 <222> LOCATION: (101)..(925)
201 <223> OTHER INFORMATION: RXA02229
203 <400> SEQUENCE: 1
204 gctggttcaa cagagaccac cgcgtgtcct gggtcgacgc ctctggcgat cccaccgcac 60
206 aagccttgga gatTTTgggt ctacaatagc gaggggtgaat ttg acc atc ccc ttt 115
207                                     Leu Thr Ile Pro Phe
208                                     1           5
210 gcc aaa ggc cac gcc acc gaa aac gac ttc atc atc atc ccc gat gag 163

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211 Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile Ile Ile Pro Asp Glu
212          10          15          20
214 gat gcg cgc cta gat tta act cca gaa atg gtg gtc acg ctg tgt gac 211
215 Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val Val Thr Leu Cys Asp
216          25          30          35
218 cgc cgc gcc ggg atc ggt gct gat ggt atc ctc cgc gtg gtt aaa gct 259
219 Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu Arg Val Val Lys Ala
220          40          45          50
222 gca gac gta gaa ggc tcc acg gtc gac cca tcg ctg tgg ttc atg gat 307
223 Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser Leu Trp Phe Met Asp
224          55          60          65
226 tac cgc aac gcc gat gga tct ttg gct gaa atg tgc ggc aat ggt gtg 355
227 Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met Cys Gly Asn Gly Val
228          70          75          80          85
230 cgc ctg ttc gcg cac tgg ctg tac tcc cgc ggt ctt gtt gat aat acg 403
231 Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly Leu Val Asp Asn Thr
232          90          95          100
234 agc ttt gat atc ggt acc cgc gcc ggt gtc cgc cac gtt gat att ttg 451
235 Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg His Val Asp Ile Leu
236          105          110          115
238 cag gca gat caa cat tct gcg cag gtc cgc gtt gat atg ggc atc cct 499
239 Gln Ala Asp Gln His Ser Ala Gln Val Arg Val Asp Met Gly Ile Pro
240          120          125          130
242 gac gtc acg gga tta tcc acc tgc gac atc aac ggc caa gta ttc gct 547
243 Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn Gly Gln Val Phe Ala
244          135          140          145
246 ggc ctt ggc gtt gat atg ggt aac cca cac cta gcg tgc gtt gtg ccg 595
247 Gly Leu Gly Val Asp Met Gly Asn Pro His Leu Ala Cys Val Val Pro
248          150          155          160          165
250 ggc tta agt gcg tcg gct ctt gcc gat atg gaa ctg cgc gca cct acg 643
251 Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu Leu Arg Ala Pro Thr
252          170          175          180
254 ttt gat cag gaa ttc ttc ccc cac ggt gtg aac gta gaa atc gtc aca 691
255 Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn Val Glu Ile Val Thr
256          185          190          195
258 gaa tta gaa gat gac gca gta tcg atg cgc gtg tgg gaa cgc gga gtg 739
259 Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val Trp Glu Arg Gly Val
260          200          205          210
262 ggc gaa acc cgc tcc tgt ggc acg gga acc gtt gct gca gcg tgt gct 787
263 Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val Ala Ala Ala Cys Ala
264          215          220          225
266 gct tta gct gat gct gga ttg gga gaa ggc aca gct aaa gtg tgc gtt 835
267 Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr Ala Lys Val Cys Val
268          230          235          240          245
270 cca cgt ggg gaa gta gaa gtc cag atc ttt gac gac ggc tcc aca ctc 883
271 Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp Asp Gly Ser Thr Leu
272          250          255          260
274 acc ggc cca agc gcc atc atc gca ctc ggt gag gtg cag atc 925
275 Thr Gly Pro Ser Ala Ile Ile Ala Leu Gly Glu Val Gln Ile

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276          265          270          275          948
278 taagattcgc gattgtagtt cgg
281 <210> SEQ ID NO: 2
282 <211> LENGTH: 275
283 <212> TYPE: PRT
284 <213> ORGANISM: Corynebacterium glutamicum
286 <400> SEQUENCE: 2
287 Leu Thr Ile Pro Phe Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile
288   1          5          10          15
290 Ile Ile Pro Asp Glu Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val
291          20          25          30
293 Val Thr Leu Cys Asp Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu
294          35          40          45
296 Arg Val Val Lys Ala Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser
297          50          55          60
299 Leu Trp Phe Met Asp Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met
300   65          70          75          80
302 Cys Gly Asn Gly Val Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly
303          85          90          95
305 Leu Val Asp Asn Thr Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg
306          100          105          110
308 His Val Asp Ile Leu Gln Ala Asp Gln His Ser Ala Gln Val Arg Val
309          115          120          125
311 Asp Met Gly Ile Pro Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn
312          130          135          140
314 Gly Gln Val Phe Ala Gly Leu Gly Val Asp Met Gly Asn Pro His Leu
315 145          150          155          160
317 Ala Cys Val Val Pro Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu
318          165          170          175
320 Leu Arg Ala Pro Thr Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn
321          180          185          190
323 Val Glu Ile Val Thr Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val
324          195          200          205
326 Trp Glu Arg Gly Val Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val
327          210          215          220
329 Ala Ala Ala Cys Ala Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr
330 225          230          235          240
332 Ala Lys Val Cys Val Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp
333          245          250          255
335 Asp Gly Ser Thr Leu Thr Gly Pro Ser Ala Ile Ile Ala Leu Gly Glu
336          260          265          270
338 Val Gln Ile
339          275
342 <210> SEQ ID NO: 3
343 <211> LENGTH: 1491
344 <212> TYPE: DNA
345 <213> ORGANISM: Corynebacterium glutamicum
347 <220> FEATURE:
348 <221> NAME/KEY: CDS

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/606,740A

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Input Set : F:\seqlistcorrected.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:69; N Pos. 57  
Seq#:81; Xaa Pos. 187,188,209,212  
Seq#:82; Xaa Pos. 187,188,209,212  
Seq#:199; N Pos. 598,676,687,690,691,693  
Seq#:199; Xaa Pos. 192,196,197,198  
Seq#:200; Xaa Pos. 192,196,197,198  
Seq#:311; N Pos. 640,641,642,643,644,645,646,647  
Seq#:311; Xaa Pos. 181,182,183  
Seq#:312; Xaa Pos. 181,182,183  
Seq#:339; N Pos. 863  
Seq#:339; Xaa Pos. 255  
Seq#:340; Xaa Pos. 255  
Seq#:341; N Pos. 94  
Seq#:805; N Pos. 409,421  
Seq#:805; Xaa Pos. 96,99,106,107,109,110,112,114,115,116  
Seq#:806; Xaa Pos. 96,99,106,107,109,110,112,114,115,116  
Seq#:915; N Pos. 120  
Seq#:915; Xaa Pos. 33  
Seq#:916; Xaa Pos. 33  
Seq#:1029; N Pos. 850,853  
Seq#:1031; N Pos. 71,74,155,162,192,211,214,225,230,233  
Seq#:1031; Xaa Pos. 19,21,31,42,44,45  
Seq#:1032; Xaa Pos. 19,21,31,42,44,45  
Seq#:1069; N Pos. 504,535  
Seq#:1069; Xaa Pos. 168,179  
Seq#:1070; Xaa Pos. 168,179

## VERIFICATION SUMMARY

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Input Set : F:\seqlistcorrected.txt

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L:6088 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69 after pos.:0  
L:7780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81 after pos.:691  
L:7784 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81 after pos.:739  
L:7851 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:176  
L:7857 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:208  
L:17306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:199 after pos.:595  
L:17310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:199 after pos.:643  
L:17311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:199 after pos.:691  
L:17314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:199 after pos.:691  
L:17315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:199 after pos.:703  
L:17378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:200 after pos.:176  
L:17381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:200 after pos.:192  
L:27412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:311 after pos.:595  
L:27413 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:311 after pos.:643  
L:27416 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:311 after pos.:643  
L:27417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:311 after pos.:691  
L:27674 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:312 after pos.:176  
L:30146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:339 after pos.:835  
L:30147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:339 after pos.:883  
L:30209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:340 after pos.:240  
L:30234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:341 after pos.:60  
L:66296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:805 after pos.:403  
L:66299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:805 after pos.:403  
L:66300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:805 after pos.:451  
L:66385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:806 after pos.:80  
L:66388 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:806 after pos.:96  
L:66391 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:806 after pos.:112  
L:74931 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:915 after pos.:100  
L:74932 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:915 after pos.:148  
L:75001 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:916 after pos.:32  
L:84158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1029 after pos.:835  
L:84266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1031 after pos.:60  
L:84270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1031 after pos.:115  
L:84271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1031 after pos.:163  
L:84274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1031 after pos.:163  
L:84275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1031 after pos.:211  
L:84278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1031 after pos.:211  
L:84279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1031 after pos.:259  
L:84321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1032 after pos.:16  
L:84324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1032 after pos.:32  
L:87276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1069 after pos.:480  
L:87277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1069 after pos.:528  
L:87280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1069 after pos.:528  
L:87281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1069 after pos.:576  
L:87397 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1070 after pos.:160  
L:87400 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1070 after pos.:176